

EXHIBIT A

JAN 1 3 2005

MPI93-006CP1DV1ACN1DV1M

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| Sundelin, Johan, et al.  |            |             |
| 10/643,627   | Group No.: | 1636        |
| August 19, 2003  | Examiner:  | Guzo, David |
| RECOMBINANT C140 RECEPTOR ITS AGONISTS AND ANTAGONISTS,<br>AND NUCLEIC ACIDS ENCODING THE RECEPTOR |            |             |

Alignment of polypeptide sequences of SEQ ID 4 and SEQ ID 63  
 SEQ ID 4 398 aa vs. SEQ ID 63 397 aa

ALIGN calculates a global alignment of two sequences  
 version 2.0uPlease cite: Myers and Miller, CABIOS (1989)  
 scoring matrix: BLOSUM50, gap penalties: -12/-2  
 91.8% identity; Global alignment score: 2342

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      10      20      30      40      50
/tmp/s MNVLSFEQTSVTAETFISVMTLVFLSCTGT----NRSSKGRSLIGKVDGTSHVTKGVTV
      :      :      :      :      :
SEQ    M-----RSPSAWLLGAAILLAAASLSCSGTIQGTNRSSKGRSLIGKVDGTSHVTKGVTV
      10      20      30      40      50

      60      70      80      90      100     110
/tmp/s ETVFSVDEFSASVLTGKLTTVFLPIVYTIVFVVGLPSNGMALWVFLFRTRKKHPAVIYMA
      :      :      :      :      :
SEQ    ETVFSVDEFSASVLAGKLTTVFLPIVYTIVFAVGLPSNGMALWVFLFRTRKKHPAVIYMA
      60      70      80      90      100     110

      120     130     140     150     160     170
/tmp/s NLALADLLSVIWFPLKIAYHIHGNNIYGEALCNVLIGFFYGNMYCSILFMTCLSVQRYW
      :      :      :      :      :
SEQ    NLALADLLSVIWFPLKIAYHIHGNNIYGEALCNVLIGFFYRNMYCSILFMTCLSVQRYW
      120     130     140     150     160     170

      180     190     200     210     220     230
/tmp/s VIVNPMGHSRKKKANIAIGISLAIWLLILLVTIPLYVVKQTIFIPALNITTCHDVLPEQLL
      :      :      :      :      :
SEQ    VIVNPMGHSRKKKANIAIGISLAIWLLTLLVTIPLYVVKQTIFIPALNITTCHDVLPEQLL
      180     190     200     210     220     230

      240     250     260     270     280     290
/tmp/s VGDMFNYYFLSLAIGVFLPAAFLTASAYVLMIRMLRSSAMENSEKKRKRAIKLIVTVLAM
      :      :      :      :      :
SEQ    VGDMFNYYFLSLAIGVFLPAAFLTASAYVLMIRMLRSSAMENSEKKRKRAIKLIVTVLGM
      240     250     260     270     280     290

      300     310     320     330     340     350
/tmp/s YLICFTPSNLLLVVHYFLIKSQGQSHVYALYIVALCLSTLNCSIDPFVYYFVSHDFRDHA
      :      :      :      :      :
SEQ    YLICFTPSNLLLVVHYFLIKSQGQSHVYALYIVALCLSTLNCSIDPFVYYFVSHDFRDHA
      300     310     320     330     340     350

      360     370     380     390
/tmp/s KNALLCRSVRTVKQMQLVPLTSKKHSRKSSSYSSSTTVKTSY
      :      :      :
SEQ    KNALLCRSVRTVKQMQLVPLTSKKHSRKSSSYSSSTTVKTSY
      360     370     380     390

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